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TECH CENTER 1600/2900

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/313,942

DATE: 02/14/2002
TIME: 15:49:04

ENTERED

Input Set : A:\REG203.txt
Output Set: N:\CRF3\02142002\I313942.raw

```
 4 <110> APPLICANT: REGENERON PHARMACEUTICALS, INC.
 6 <120> TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 7       AND USING
 9 <130> FILE REFERENCE: REG 203-A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/313,942
12 <141> CURRENT FILING DATE: 1999-05-19
14 <150> PRIOR APPLICATION NUMBER: 09/313,942
15 <151> PRIOR FILING DATE: 1999-05-19
17 <150> PRIOR APPLICATION NUMBER: 60/101,858
18 <151> PRIOR FILING DATE: 1998-09-25
20 <160> NUMBER OF SEQ ID NOS: 32
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 6
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Tag sequence
32 <400> SEQUENCE: 1
33   His His His His His His
34   1               5
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 16
38 <212> TYPE: PRT
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: peptide derived from region near C-terminus of
43       gp130
45 <400> SEQUENCE: 2
46   Cys Gly Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu
47   1               5                   10                  15
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 16
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Kozak sequence
57 <400> SEQUENCE: 3
58   cgccgccacc atggtg                                      16
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 10
62 <212> TYPE: PRT
63 <213> ORGANISM: Artificial Sequence
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OK to Enter

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65 <220> FEATURE:
66 <223> OTHER INFORMATION: J peptide
68 <400> SEQUENCE: 4
69 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
70 1   5   10
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 11
74 <212> TYPE: PRT
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: J peptide
80 <400> SEQUENCE: 5
81 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
82 1   5   10
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 10
86 <212> TYPE: PRT
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: linker sequence
92 <400> SEQUENCE: 6
93 Gly Ala Pro Ser Gly Gly Gly Gly Arg Pro
94 1   5   10
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 859
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 7
102 Met Val Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu
103 1   5   10   15
104 Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
105   20   25   30
106 Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
107   35   40   45
108 Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
109   50   55   60
110 Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
111 65   70   75   80
112 Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
113   85   90   95
114 Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
115   100   105   110
116 Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
117   115   120   125
118 Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
119   130   135   140
120 Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
121 145   150   155   160
122 Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg

```
123                165              170                175
124  Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
125        180              185              190
126  Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
127        195              200              205
128  Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
129        210              215              220
130  Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
131  225              230              235              240
132  Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
133        245              250              255
134  Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
135        260              265              270
136  Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
137        275              280              285
138  Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
139        290              295              300
140  Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
141  305              310              315              320
142  Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
143        325              330              335
144  Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
145        340              345              350
146  Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
147        355              360              365
148  Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
149        370              375              380
150  Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
151  385              390              395              400
152  Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
153        405              410              415
154  Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
155        420              425              430
156  Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
157        435              440              445
158  Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
159        450              455              460
160  Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
161  465              470              475              480
162  Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
163        485              490              495
164  Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
165        500              505              510
166  Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
167        515              520              525
168  Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
169        530              535              540
170  Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
171  545              550              555              560
```

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```
172  Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
173              565                 570             575
174  Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
175              580                 585             590
176  Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
177              595                 600             605
178  Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ser Gly Glu Pro Lys
179              610                 615             620
180  Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
181  625              630                 635             640
182  Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
183              645                 650             655
184  Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
185              660                 665             670
186  Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
187              675                 680             685
188  Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
189      690                 695             700
190  Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
191  705                 710             715                 720
192  Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
193              725                 730             735
194  Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
195              740                 745             750
196  Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
197              755                 760             765
198  Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
199      770                 775             780
200  Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
201  785                 790             795                 800
202  Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
203              805                 810             815
204  Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
205              820                 825             830
206  Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
207          835                 840                 845
208  Leu Ser Pro Gly Lys His His His His His His
209          850                 855
211 <210> SEQ ID NO: 8
212 <211> LENGTH: 592
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens
216 <400> SEQUENCE: 8
217  Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
218  1                5                 10                  15
219  Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
220              20                  25                  30
221  Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
222              35                  40                  45
```

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```
223   Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
224       50                      55                  60
225   Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
226   65                      70                  75                  80
227   Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
228                   85                  90                  95
229   Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
230                   100                 105                 110
231   Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
232               115                 120                 125
233   Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
234       130                     135                 140
235   Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
236   145                     150                 155                 160
237   Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
238                   165                 170                 175
239   Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
240                   180                 185                 190
241   Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
242               195                 200                 205
243   Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
244       210                     215                 220
245   Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
246   225                     230                 235                 240
247   Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
248                   245                 250                 255
249   Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
250               260                 265                 270
251   Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
252               275                 280                 285
253   Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
254       290                     295                 300
255   Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
256   305                     310                 315                 320
257   Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
258                   325                 330                 335
259   Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr
260               340                 345                 350
261   Ser Leu Pro Val Gln Asp Ala Gly Glu Pro Lys Ser Cys Asp Lys Thr
262               355                 360                 365
263   His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
264       370                     375                 380
265   Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
266   385                     390                 395                 400
267   Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
268               405                 410                 415
269   Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
270               420                 425                 430
271   Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
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VERIFICATION SUMMARY
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Input Set : A:\REG203.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number